

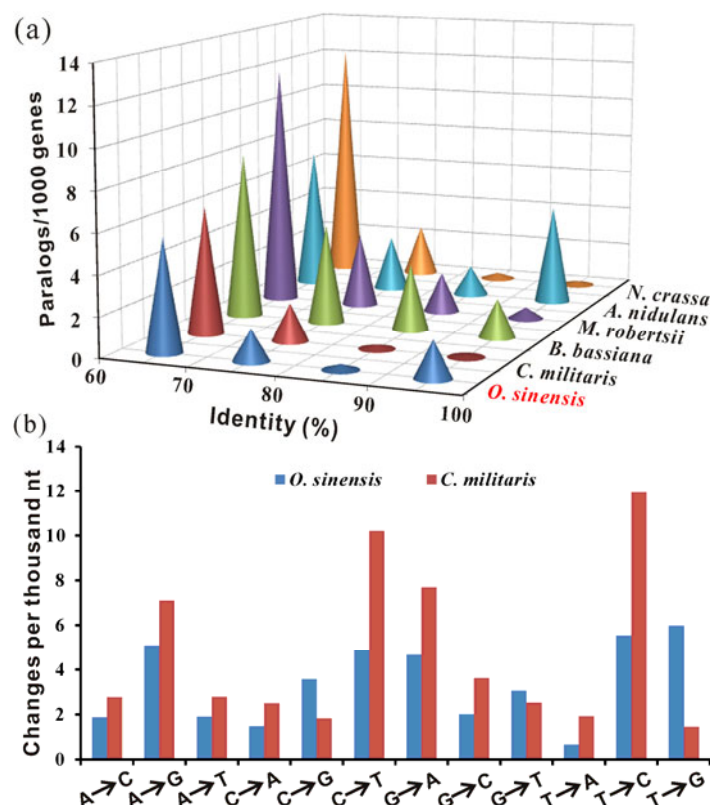


Figure S1 Analysis of repeat-induced point mutation (RIP) in *O. sinensis*. RIP is a fungal genome defense mechanism guarding against transposon invasion. RIP mutates the sequence of repeated DNA introducing a C:G to T:A mutation bias. (a) Distribution of paralogous gene numbers with different level of nucleotide similarity in *O. sinensis* and other fungi. We found 12 pairs with > 90% nucleotide sequence similarities in *O. sinensis* in contrast to only one pair each in RIP-effective species *Neurospora crassa* and *Cordyceps militaris*. (b) Analysis and comparison of nucleotide mutation rates of the paired *O. sinensis* and *C. militaris* genes showing >80% nucleotide identities. In contrast to *C. militaris*, *O. sinensis* lacks the C:G to T:A mutation bias characteristic of RIP.

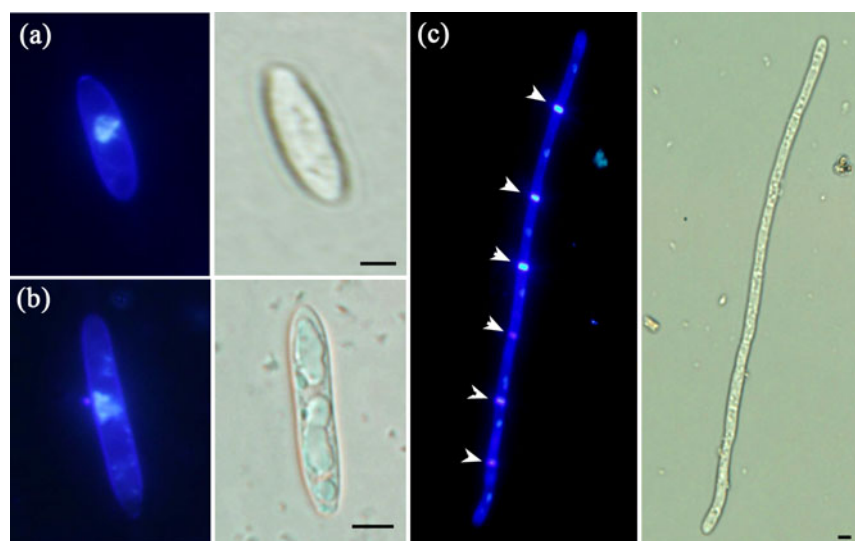


Figure S2 Examination of the number of nuclei in *O. sinensis* cells harvested from liquid culture. The cells were double stained with the Calcofluor White and 4',6-diamidino-2-phenylindole (DAPI). Panels (a), (b) and (c) show a yeast-like blastospore, a bar-shaped blastospore and mycelium, respectively. Arrows in Panel (c) point to a hyphal septum. The right panels show bright field images. Bar, 5 μm.

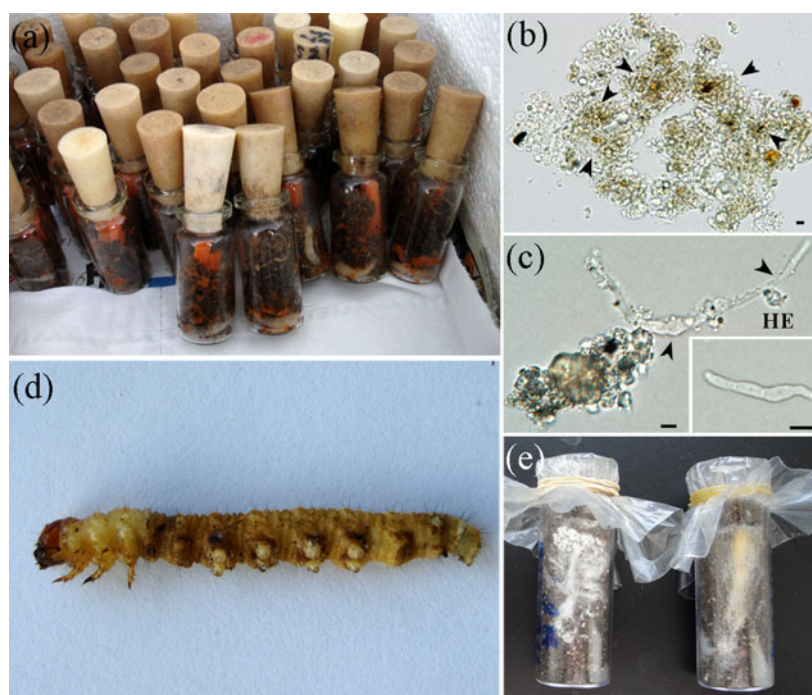


Figure S3 Failure to induce *O. sinensis* fruiting-body production in the laboratory. (a) Late instar larvae of ghost moth caterpillars were injected with 10 µl of fungal cells (1×10^7 cells per ml of water). (b) Spores were encapsulated and melanized (arrowed) by insect hemocytes 24 hours post injection. (c) Three weeks post infection, fungal cells (arrowed) were found growing within the treated insect hemocoel but not in insects from the control experiment. Inset: fungal cells observed in a newly killed insect one month post injection. Bar, 5 µm. (d) A dead insect colonized by *O. sinensis*. (e) Insect cadavers incubated in soil for up to three months failed to produce fruiting bodies. Left sample first treated at 4 °C for one month and then two months at 18 °C; Right sample treated for three months at 18 °C.

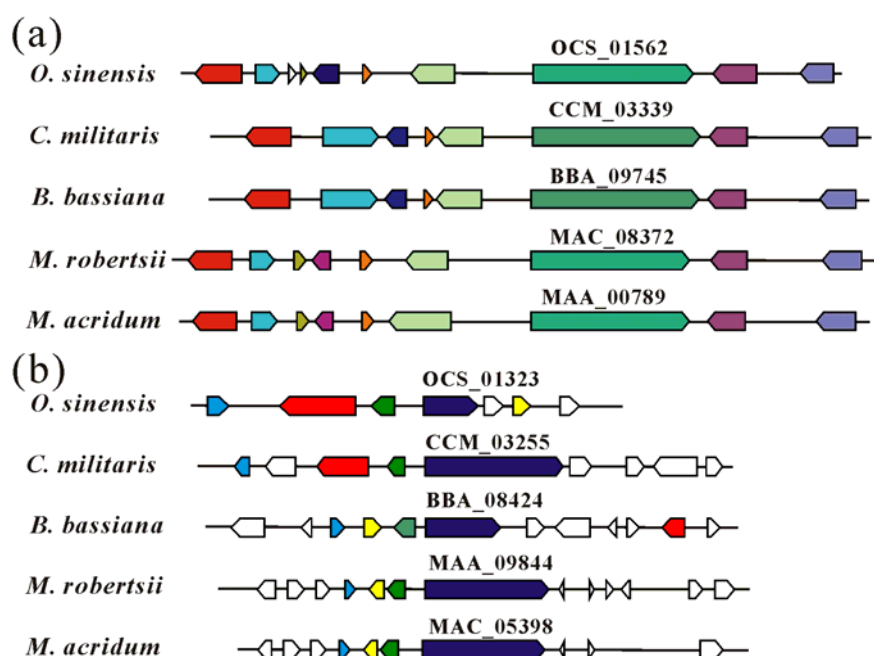


Figure S4 Syntenic relationship analysis of gene clusters involved in the biosynthesis of different secondary metabolites between *O. sinensis* and other insect pathogens. (a) A polyketide synthase gene (OCS_01562) cluster, and (b) a non-ribosomal peptide synthetase gene (OCS_01323) cluster is conserved in four insect pathogens. In each panel, orthologous genes are labeled in the same color. The genes labeled in white are orphans.

Table S1 The single ascospore isolates used for mating type characterization

Ser. No.	Isolate No.	Collection source
1	XZ49-1	Changdu, Tibet
2	XZ49-2	Changdu, Tibet
3	XZ49-3	Changdu, Tibet
4	XZ49-4	Changdu, Tibet
5	XZ49-5	Changdu, Tibet
6	XZ49-6	Changdu, Tibet
7	XZ49-7	Changdu, Tibet
8	XZ49-8	Changdu, Tibet
9	XZ49-9	Changdu, Tibet
10	XZ49-10	Changdu, Tibet
11	XZ49-11	Changdu, Tibet
12	XZ49-12	Changdu, Tibet
13	XZ49-13	Changdu, Tibet
14	XZ51-1	Changdu, Tibet
15	XZ51-2	Changdu, Tibet
16	XZ51-3	Changdu, Tibet
17	XZ51-4	Changdu, Tibet
18	XZ51-5	Changdu, Tibet
19	XZ51-6	Changdu, Tibet
20	QH195-2	Yushu, Qinhai
21	XZ36-3	Changdu, Tibet
22	XZ36-4	Changdu, Tibet
23	XZ36-5	Changdu, Tibet
24	XZ36-6	Changdu, Tibet
25	XZ157-1	Naqu, Tibet
26	XZ157-2	Naqu, Tibet
27	XZ157-3	Naqu, Tibet
28	XZ157-4	Naqu, Tibet
29	XZ157-5	Naqu, Tibet
30	XZ157-6	Naqu, Tibet
31	XZ157-7	Naqu, Tibet
32	XZ157-8	Naqu, Tibet
33	XZ157-9	Naqu, Tibet
34	XZ157-10	Naqu, Tibet
35	XZ157-11	Naqu, Tibet
36	XZ157-12	Naqu, Tibet
37	XZ157-13	Naqu, Tibet
38	XZ157-14	Naqu, Tibet
39	XZ157-15	Naqu, Tibet
40	XZ157-16	Naqu, Tibet
41	XZ141-1	Naqu, Tibet
42	XZ141-2	Naqu, Tibet
43	XZ141-3	Naqu, Tibet
44	XZ141-4	Naqu, Tibet
45	XZ141-5	Naqu, Tibet
46	XZ141-6	Naqu, Tibet
47	XZ141-7	Naqu, Tibet
48	XZ141-8	Naqu, Tibet

Table S2 Repeat rate analysis of *O. sinensis* genome-sequencing data

	Number	Length	Repeat number	Repeat length	No. ratio (%)	Length ratio (%)
Short contigs	3,346,441	93,452,497	1,565,042	43,214,452	46.76	46.24
Long contigs	48,133	20,840,395	651	202,264	1.35	0.97
Total	3,394,574	114,292,892	1,565,693	43,416,716	46.12	37.98

Table S3 Repeat-masking analysis of the assembled *O. sinensis* genome

Class	No.	Ratio (% of total No.)
DNA/En-Spm	1	0.0030
DNA/Harbinger	33	0.0983
DNA/hAT-Tip100	2	0.0060
DNA/Helitron	2	0.0060
DNA/IS4EU	4	0.0119
DNA/MuDR	276	0.8223
DNA/P	12	0.0358
DNA/TcMar-Fot1	147	0.4380
DNA/TcMar-Marin	35	0.1043
DNA/TcMar-Pogo	28	0.0834
DNA/TcMar-Tc1	28	0.0834
DNA/TcMar-Tc2	8	0.0238
DNA/TcMar-Tigge	1	0.0030
LINE/CR1	36	0.1073
LINE/I	1	0.0030
LINE/Jockey	47	0.1400
LINE/L1	7	0.0209
LINE/L2	43	0.1281
LINE/LOA	14	0.0417
LINE/Penelope	9	0.0268
LINE/R1	19	0.0566
LINE/R2	5	0.0149
LINE/Rex-Babar	1	0.0030
LINE/RTE-BovB	9	0.0268
LINE/Tad1	1365	4.0667
LTR/Copia	8353	24.8860
LTR/Delta	1	0.0030
LTR/ERV1	50	0.1490
LTR/ERVK	9	0.0268
LTR/ERVL	1	0.0030
LTR/Foamy	6	0.0179
LTR/Gypsy	15357	45.7530
LTR/Lenti	1	0.0030
LTR/Pao	8	0.0238
RC/Helitron	239	0.7121
Tandem repeats	7407	22.0676

Table S4 Comparison of pseudogene numbers in *O. sinensis* and other insect pathogens

Pseudogene type	<i>O. sinensis</i>	<i>C. militaris</i>	<i>B. bassiana</i>	<i>M. robertsii</i>	<i>M. acridum</i>
DUP	143	9	72	129	254
PSSD	111	0	62	122	104
FRAG	856	139	170	112	82
Total	1,110	148	304	363	440

Note: DUP, duplicated pseudogenes; PSSD, processed (retrotransposed) pseudogenes; FRAG, fragmented pseudogenes.

Table S5 Sexuality-related genes functionally verified in *A. nidulans* and *N. crassa*, and their putative orthologs in *O. sinensis* and other insect pathogens

Function	<i>A. nidulans</i>	<i>N. crassa</i>	<i>O. sinensis</i>	<i>C. militaris</i>	<i>B. bassiana</i>	<i>M. robertsii</i>	<i>M. acridum</i>
Mating process							
Mating-type MAT1-1-1 (MatB)	AN2755	NCU01958	OCS_06642	CCM_06523	BBA_07733	MAA_03718	
Mating-type MAT1-1-2			OCS_06643	CCM_09679		MAA_10977	
Mating-type MAT1-1-3			OCS_06644			MAA_03719	
Mating-type MAT1-2-1 (MatA)	AN4734	NCU01960	OCS_00196				MAC_05350
Carboxypeptidase alpha-factor processing	AN1384	NCU04316	OCS_02355	CCM_02046	BBA_04810	MAA_02969	MAC_03847
Endoprotease for alpha-factor processing	AN3583	NCU03219	OCS_02254	CCM_04990	BBA_09698	MAA_05263	MAC_02797
Dipeptidyl aminopeptidase alpha-factor processing	AN2946	NCU02515	OCS_03713	CCM_07274	BBA_07034	MAA_03364	MAC_07820
Dipeptidyl aminopeptidase for a-factor processing	AN8044	NCU00481	OCS_02388	CCM_02661	BBA_04103	MAA_05780	MAC_03112
CAAX prenyl protease a-factor C-terminal processing	AN6528	NCU11314	OCS_03088	CCM_05829	BBA_08336		MAC_01887
CAAX-farnesyltransferase beta subunit; a-factor modification	AN2002	NCU05999	OCS_03113	CCM_05066	BBA_03884	MAA_02158	MAC_02644
CAAX-farnesyltransferase alpha subunit	AN6162	NCU00034	OCS_06299	CCM_05030	BBA_01915	MAA_07087	MAC_07177
ATP-dependent efflux pump for a-factor like pheromone	AN2300	NCU07546	OCS_03625	CCM_00623	BBA_08160	MAA_05864	MAC_03697
Mating signaling							
Alpha-subunit G protein	AN0651	NCU06493	OCS_06305	CCM_07236	BBA_01892	MAA_03488	MAC_04984
Beta-subunit G protein	AN0081	NCU00440	OCS_04898	CCM_09461	BBA_03738	MAA_02470	MAC_01638
Gamma-subunit G protein	AN2742	NCU00041	OCS_06260	CCM_01794	BBA_05932	MAA_05991	MAC_08659
Mitogen-activated protein kinase	AN3719	NCU02393	OCS_04717	CCM_01235	BBA_01244	MAA_04503	MAC_00098
Pheromone adaptation feedback response	AN7252	NCU00455	OCS_06899	CCM_09426	BBA_03777	MAA_02467	MAC_01635
Pheromone Receptor (for a-factor like pheromone)	AN7743	NCU00138	OCS_06804	CCM_01499	BBA_04271	MAA_05941	MAC_00610
Pheromone Receptor (for alpha-factor like pheromone)	AN2520	NCU05758	OCS_05165	CCM_06752	BBA_04483	MAA_00341	MAC_02467
Serine/threonine protein kinase MKK	AN3422	NCU04612	OCS_00626	CCM_05558	BBA_04254	MAA_04421	MAC_02314
Serine/threonine protein kinase MKKK	AN2269	NCU06182	OCS_04114	CCM_07511	BBA_02280	MAA_03529	MAC_05029
Serine/threonine protein kinase MKKKK	AN2067	NCU03894	OCS_01179	CCM_05107	BBA_07438	MAA_02118	MAC_02685
Transcriptional Activator, homeodomain DNA binding	AN2290	NCU00340	OCS_04523	CCM_01444	BBA_01078	MAA_05929	MAC_00598
Karyogamy and meiosis							
1,3-beta-glucan synthase subunit, Sp Mei4 target gene	AN3729	NCU06871	OCS_05817	CCM_01185	BBA_10207	MAA_04456	MAC_01688
ABC transporter required fo a-factor transport	AN2300	NCU07546	OCS_03625	CCM_00623	BBA_08160	MAA_05864	MAC_03697
Amino acid permease involved in sexual differentiation	AN5678	NCU05830	OCS_02119	CCM_08184	BBA_00594	MAA_04108	MAC_08710
APC component	AN0905	NCU00494	OCS_04067	CCM_07395	BBA_08125	MAA_03573	MAC_08351
APC component	AN2772	NCU05901	OCS_05008	CCM_01001	BBA_01542	MAA_04652	MAC_09483
APC component	AN4735	NCU01963	OCS_00199	CCM_06526	BBA_07736	MAA_03722	MAC_05347
APC component	AN8013	NCU01174	OCS_02500	CCM_03205	BBA_02533	MAA_09174	MAC_05975
APC component, bimA	AN6138	NCU00217	OCS_06191	CCM_07521	BBA_02267	MAA_03443	MAC_02516
APC regulator	AN0814	NCU02616	OCS_02978	CCM_05397	BBA_01439	MAA_00735	MAC_06221
APC regulator	AN2965	NCU01269	OCS_04570	CCM_03958	BBA_07253	MAA_03661	MAC_06443
ARN family of transporters for siderophore-iron chelates	AN5378		OCS_04427	CCM_08779	BBA_07619	MAA_06654	MAC_09677

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Function	<i>A. nidulans</i>	<i>N. crassa</i>	<i>O. sinensis</i>	<i>C. militaris</i>	<i>B. bassiana</i>	<i>M. robertsii</i>	<i>M. acridum</i>
bZip TF, involved in regulation of meiosis	AN6849		OCS_05442	CCM_09124	BBA_04813	MAA_02972	MAC_08931
Calmodulin-dependent protein kinase	AN3065	NCU02283	OCS_03191	CCM_01313	BBA_00508	MAA_04599	MAC_04622
Chitin synthase, pheromone inducible	AN4566	NCU04251	OCS_04853	CCM_08511	BBA_03590	MAA_03168	MAC_08014
Chromosome segregation, kinetochore-associated Ndc80	AN4969	NCU03899	OCS_03932	CCM_00302	BBA_03433	MAA_02015	MAC_03415
Cohesin	AN6364	NCU07554	OCS_01053	CCM_01887	BBA_01045	MAA_05900	MAC_03734
Phosphocholine cytidyltransferase	AN1357	NCU03880	OCS_00305	CCM_08417	BBA_06142	MAA_00035	MAC_07726
C-type cyclin	AN2172	NCU01563	OCS_02857	CCM_01137	BBA_04475	MAA_05354	MAC_01841
Cyclin-like protein interacts with Sc Pho85	AN4984	NCU07293	OCS_03462	CCM_07026	BBA_04435	MAA_03884	MAC_04184
Cytochrome-c oxidoreductase	AN3901	NCU08272	OCS_05124	CCM_02991	BBA_06880	MAA_01131	MAC_06772
DNA-binding helix-hairpin-helix protein	AN1237	NCU02741	OCS_03384	CCM_06822	BBA_02058	MAA_04013	MAC_04218
Dynactin complex, homologue of Sc NIP100	AN6323	NCU03483	OCS_04663	CCM_04587	BBA_05442	MAA_08863	MAC_07228
ER associated glutathione S-transferase	AN0629	NCU05706	OCS_02316	CCM_01615	BBA_03252	MAA_08951	MAC_06695
Fork head domain TF, meiotic regulator	AN8858	NCU06173	OCS_06910	CCM_02646	BBA_04116	MAA_05810	MAC_03141
Formin	AN6523	NCU01431	OCS_02615	CCM_07806	BBA_06491	MAA_01475	MAC_03937
GEF involved in conjugation; related to Sc CDC25	AN2130	NCU06500	OCS_06187	CCM_05772	BBA_06377	MAA_03615	MAC_06489
Glucosamine acetyl transferase involved in cell cycle progression	AN8706	NCU01902	OCS_05808	CCM_06566	BBA_02625	MAA_08730	MAC_05880
GTP binding (alpha-1 subunit) involved in conjugation	AN3090	NCU06729	OCS_06648	CCM_00555	BBA_06035	MAA_05603	MAC_01131
Hect domain E3 ubiquitin-protein ligase	AN0444	NCU06756	OCS_03053	CCM_04538	BBA_05494	MAA_07661	MAC_06530
HMG-box TF, target of pheromone signaling	AN3667	NCU09387	OCS_06292	CCM_06680	BBA_10247	MAA_00248	MAC_04576
Holliday junction resolvase	AN3118	NCU07457	OCS_04743	CCM_06887	BBA_02088	MAA_03931	MAC_05298
Inducer of meiosis, S/T kinase	AN6243	NCU01498	OCS_02952	CCM_02359	BBA_00996	MAA_05403	MAC_01790
involved in Meiosis II nuclear division, Sp Mei4 target gene	AN3931	NCU02540	OCS_04125	CCM_06283	BBA_09711	MAA_04211	MAC_03800
kinesin-like motor required for karyogamy	AN6340	NCU04581	OCS_02056	CCM_05847	BBA_08352	MAA_04756	MAC_02000
Long chain fatty acid elongation enzyme	AN8117	NCU06694	OCS_02273	CCM_03752	BBA_04877	MAA_07869	MAC_05925
MADS-box domain TF, pheromone receptor activator	AN8676	NCU07430	OCS_04793	CCM_03292	BBA_06763	MAA_07379	MAC_00861
Mating-type M-specific polypeptide Mc, HMG-box TF	AN1962	NCU03481	OCS_05413	CCM_04586	BBA_05443	MAA_10631	MAC_07229
Meiosis-specific transcriptional activator	AN6015	NCU09915	OCS_01689	CCM_04034	BBA_05141	MAA_06439	MAC_08428
Meiotic B-type cyclin	AN2137	NCU01242	OCS_06428	CCM_05610	BBA_00832	MAA_07313	MAC_00492
M-factor farnesyl cysteine carboxyl methyltransferase	AN6162	NCU00034	OCS_06300	CCM_05030	BBA_01915	MAA_07087	MAC_07177
Microtubule-binding protein	AN2862	NCU00243	OCS_00496	CCM_02770	BBA_04004	MAA_09680	MAC_09803
Phosphoglucomutase	AN2867	NCU10058	OCS_02582	CCM_02278	BBA_04232	MAA_04308	MAC_03213
Polo kinase	AN1560	NCU09258	OCS_06003	CCM_06972	BBA_08042	MAA_00136	MAC_07512
P-type ATPase sodium pump	AN6642	NCU05046	OCS_04959	CCM_04844	BBA_09050	MAA_08450	MAC_06648
Ras	AN0182	NCU08823	OCS_05591	CCM_06996	BBA_04387	MAA_06380	MAC_01355
Required for autophagic vesicle delivery to vacuole	AN5131	NCU01545	OCS_05823	CCM_07484	BBA_02302	MAA_02674	MAC_08764
Meiosis-specific topoisomerase Spo11	AN8259	NCU01120	OCS_03978	CCM_09527			
Rho-GEF	AN4719	NCU00668	OCS_06478	CCM_03356	BBA_07881	MAA_07421	MAC_00815
Riboflavin synthase, alpha subunit	AN4231	NCU07456	OCS_04744	CCM_06886	BBA_02087	MAA_03932	MAC_05297
Ribose-5-phosphate isomerase	AN2440	NCU07608	OCS_06483	CCM_00462	BBA_03239	MAA_02753	MAC_08154
RING-type ubiquitin ligase, FYVE finger domain	AN0627	NCU08974	OCS_02185	CCM_05861	BBA_08364	MAA_05768	MAC_03100
RNA binding protein required for meiotic recombination	AN9090	NCU00768	OCS_05666	CCM_03581	BBA_03049	MAA_07476	MAC_07476
RNA-binding protein involved in meiosis	AN6494	NCU00118	OCS_05556	CCM_05815	BBA_09975	MAA_03639	MAC_06466
RNA-binding protein involved in meiosis, Sp Mei4 target	AN7700	NCU00556	OCS_00350	CCM_00789	BBA_02405	MAA_03790	MAC_00971
SAM domain, similar to Sc STE50	AN7252	NCU00455	OCS_06899	CCM_09426	BBA_03777	MAA_02467	MAC_01635
Septin	AN1394	NCU03515	OCS_00123	CCM_00216	BBA_08598	MAA_02556	MAC_03632
Serine carboxypeptidase, degrades extracellular P-factor	AN2555	NCU06720	OCS_02487	CCM_01903	BBA_00850	MAA_09950	MAC_02763
Serine/threonine protein kinase, negative regulator of meiosis	AN4935	NCU04990	OCS_04406	CCM_00683	BBA_08648	MAA_09884	MAC_02282

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(Continued)

Function	<i>A. nidulans</i>	<i>N. crassa</i>	<i>O. sinensis</i>	<i>C. militaris</i>	<i>B. bassiana</i>	<i>M. robertsii</i>	<i>M. acridum</i>
SH3-domain protein	AN2995	NCU00696	OCS_00737	CCM_00772	BBA_02425	MAA_03765	MAC_07579
Spindle pole body component	AN5521	NCU04535	OCS_01011	CCM_00173	BBA_08305	MAA_05499	MAC_07346
Spindle pole body component	AN5618	NCU09871	OCS_00102	CCM_04480	BBA_02843	MAA_02280	MAC_03427
Spliceosome component	AN1861	NCU00361	OCS_01066	CCM_01429	BBA_01066	MAA_05886	MAC_03719
Sporulation regulated septin	AN4667	NCU02464	OCS_02832	CCM_05213	BBA_05547	MAA_10305	MAC_04367
Sporulation regulated septin	AN8182	NCU03795	OCS_06471	CCM_09142	BBA_04748	MAA_07332	MAC_00472
Sporulation-specific enzyme required for spore wall maturation	AN2705		OCS_04544	CCM_01728	BBA_09587	MAA_09988	MAC_08553
ubiquitin-conjugating enzyme, chromosome segregation	AN5495	NCU11509	OCS_01386	CCM_05530	BBA_00216	MAA_00522	MAC_07614
Vacuolar ATPase Ca ²⁺ pump	AN1189	NCU04736	OCS_01528	CCM_04692	BBA_06258	MAA_00012	MAC_02382
Xylose kinase	AN8790	NCU11353	OCS_05208	CCM_09684	BBA_02252	MAA_03458	MAC_02531
Zn finger transcription factor, unknown function	AN3447	NCU05007	OCS_05234	CCM_08238	BBA_00653	MAA_06676	MAC_07713
Fruiting body development							
Binuclear zinc transcription factor	AN5170	NCU07392	OCS_05114	CCM_00123	BBA_01641	MAA_05237	MAC_05412
Cys6-Zn ² transcriptional activator	AN1848	NCU07392	OCS_02179	CCM_02196	BBA_04319	MAA_04374	MAC_06154
GATA-transcription factor	AN3152	NCU01154	OCS_03409	CCM_00560	BBA_06064	MAA_05601	MAC_01133
Modulator of pheromone-inducible gene expression	AN8676	NCU07430	OCS_04793	CCM_03292	BBA_06763	MAA_07379	MAC_00861
Mutanase, cell wall turnover during sexual development	AN7349						
Regulator of myosin function	AN0135	NCU06821	OCS_05043	CCM_02480	BBA_09803	MAA_02633	MAC_03554
Repressor of b mating type regulated genes	AN8211	NCU01238	OCS_04623	CCM_07966	BBA_06597	MAA_01434	MAC_04053
Signalosome subunit 4, regulation of sexual development	AN1539	NCU07361	OCS_00445	CCM_08174	BBA_00583	MAA_04103	MAC_03079
Signalosome subunit 5, regulation of sexual development	AN2129	NCU00467	OCS_01205	CCM_02582	BBA_04172	MAA_08893	MAC_05426
Transcription factor	AN6230	NCU07617	OCS_05103	CCM_01634	BBA_04959	MAA_05553	MAC_01182
Velvet activator VeA	AN1052	NCU01731	OCS_04577	CCM_04531	BBA_05501	MAA_01811	MAC_00039
Cytochrome P450, required for sexual development	AN9008	NCU04834	OCS_06517	CCM_04461	BBA_02816	MAA_02298	MAC_04734

Table S6 Comparison of selected protein families between *O. sinensis* and other insect pathogens

Protein family	<i>O. sinensis</i>	<i>C. militaris</i>	<i>B. bassiana</i>	<i>M. robertsii</i>	<i>M. acridum</i>
Heterokaryon incompatibility proteins	5	15	21	34	22
Dehydrogenases	103	271	252	216	209
Cytochrome P450	57	57	83	123	100
Trypsins	2	12	23	32	17
Subtilisins	17	35	43	55	43
Aspartic proteases	12	21	21	33	25
Chitinases	9	20	20	21	14
Concanavalin A-like lectins	6	25	33	20	18
Glycoside hydrolases	66	135	145	159	130
Secondary metabolite biosynthesis backbone enzymes	28	30	42	61	40
Sugar/inositol transporters	10	3	6	5	5
Appressorium differentiation protein (MAS-like protein)	2	4	4	6	6
Adhesins	0	2	2	2	2
Chloroperoxidases	7	0	1	4	2

Table S7 Comparison of dehydrogenases encoded in the insect pathogens and plant obligate pathogen *B. graminis*

Enzyme family		EC No.	<i>O. sinensis</i>	<i>M. robertsii</i>	<i>M. acridum</i>	<i>B. bassiana</i>	<i>C. militaris</i>	<i>B. graminis</i>
Alcohol dehydrogenase	Alcohol dehydrogenase	1.1.1.1	9	27	29	23	24	2
	Alcohol dehydrogenase (NADP+)	1.1.1.2	7	26	22	19	17	5
D-xylulose reductase		1.1.1.9	2	1	1	1	0	0
Glycerate dehydrogenase		1.1.1.29	0	4	4	1	1	0
Glycerol-3-phosphate dehydrogenase(NAD+)		1.1.1.8	1	1	1	1	1	1
Glucose dehydrogenase	dTDP-4-Dehydrorhamnose reductase	1.1.1.133	1	1	1	1	1	0
	Glucose 1-dehydrogenase	1.1.1.47	3	8	8	8	8	2
	Glucose 6-phosphate dehydrogenase	1.1.1.49	1	1	1	1	1	1
	Glucose 1-dehydrogenase (NAD(+))	1.1.1.118	0	2	1	2	1	0
	Udp-glucose6-dehydrogenase	1.1.1.22	2	2	2	2	1	0
Homoserine dehydrogenase		1.1.1.3	1	1	1	1	1	1
Histidinol dehydrogenase		1.1.1.23	1	1	1	1	1	1
Sorbitol dehydrogenase (SDH)		1.1.1.14	5	7	7	4	8	1
Shikimate dehydrogenase		1.1.1.25	2	4	5	5	5	1
Lactate/Malate dehydrogenase	3-isopropylmalate dehydrogenase	1.1.1.85	0	2	2	2	2	0
	D-Lactate dehydrogenase	1.1.1.28	1	1	1	0	0	0
	L-Lactate dehydrogenase	1.1.1.27	0	1	2	1	1	0
	Malate dehydrogenase	1.1.1.37	2	2	2	2	2	2
	(R)-2-hydroxyacid dehydrogenase	1.1.1.272	0	1	0	1	1	0
3-hydroxybutyrate dehydrogenase		1.1.1.30	0	2	2	3	1	0
3-Hydroxyisobutyrate dehydrogenase		1.1.1.31	0	4	4	3	4	1
3-Hydroxyacyl-CoA dehydrogenase		1.1.1.35	5	8	7	6	6	4
Isocitrate dehydrogenase (NAD+)		1.1.1.41	1	2	2	2	2	2
Isocitrate dehydrogenase (NADP(+))		1.1.1.42	1	1	1	1	1	1
Phosphogluconate dehydrogenase		1.1.1.44	1	2	3	2	1	1
L-Gulonate 3-dehydrogenase		1.1.1.45	1	1	0	1	0	0
Hydroxysteroid Dehydrogenase (HSD)	3 Alpha-Hydroxysteroid dehydrogenase	1.1.1.50	0	2	2	1	0	1
	7-alpha-hydroxysteroid dehydrogenase	1.1.1.159	1	3	4	0	0	0
	11-beta-hydroxysteroid dehydrogenase	1.1.1.146	2	3	1	4	4	3
	estradiol 17-beta-dehydrogenase	1.1.1.62	6	11	16	14	18	2
	20-alpha-hydroxysteroid dehydrogenase	1.1.1.149	0	2	3	0	1	0
	3(or 17)-beta-hydroxysteroid dehydrogenase	1.1.1.51	0	2	0	0	0	0
	3-alpha-(or 20-beta)-hydroxysteroid dehydrogenase	1.1.1.53	3	6	5	3	3	0
Mannitol 2-dehydrogenase		1.1.1.67	0	0	0	0	0	1
Gluconate 5-dehydrogenase		1.1.1.69	5	23	17	15	15	5
Homoisocitrate dehydrogenase		1.1.1.87	0	1	1	1	1	1
Aryl-alcohol dehydrogenase		1.1.1.90	0	3	2	1	2	0
Phosphoglycerate dehydrogenase		1.1.1.95	2	6	5	7	7	2
L-Threonine-3-dehydrogenase		1.1.1.103	0	4	1	1	0	0
2-Deoxy-D-gluconate 3-dehydrogenase		1.1.1.125	0	0	1	0	0	0
GDP-Mannose 6-dehydrogenase		1.1.1.132	0	1	1	1	1	0

(To be continued on the next page)

(Continued)

Enzyme family		EC No.	<i>O. sinensis</i>	<i>M. robertsii</i>	<i>M. acridum</i>	<i>B. bassiana</i>	<i>C. militaris</i>	<i>B. graminis</i>
Mannitol dehydrogenase		1.1.1.138	0	2	3	4	3	1
15-Hydroxyprostaglandin dehydrogenase (NAD+)		1.1.1.141	0	6	3	2	1	0
IMP dehydrogenase		1.1.1.205	1	1	1	1	1	1
2-(R)-hydroxypropyl-CoM dehydrogenase		1.1.1.268	5	8	6	6	5	2
S-(hydroxymethyl)glutathione dehydrogenase		1.1.1.284	1	1	1	1	1	1
Formate Dehydrogenase		1.2.1.2	1	3	2	1	1	0
Aldehyde Dehydrogenase	Aldehyde dehydrogenase (NAD+)	1.2.1.3	2	6	5	2	2	1
	Aldehyde dehydrogenase (NAD(P)(+))	1.2.1.5	1	2	2	2	2	1
	Betaine-aldehyde dehydrogenase	1.2.1.8	1	2	4	1	1	1
	Aminobutyraldehyde dehydrogenase	1.2.1.19	0	1	1	0	0	0
	Glyceraldehyde-3-phosphate Dehydrogenase (NADP(+))	1.2.1.9	1	1	0	2	1	0
	Glyceraldehyde 3-phosphate dehydrogenase(phosphorylating)	1.2.1.12	1	1	1	1	1	1
	Lactaldehyde dehydrogenase	1.2.1.22	0	1	2	1	0	0
	Retinal dehydrogenase	1.2.1.36	0	7	5	4	6	1
Aspartate-semialdehyde dehydrogenase		1.2.1.11	0	1	1	1	1	1
Methylmalonate-semialdehyde dehydrogenase		1.2.1.27	1	1	1	1	1	1
N-acetyl-gamma-glutamyl-phosphate reductase		1.2.1.38	1	1	2	2	2	1
Glutamate 5-Semialdehyde		1.2.1.41	0	1	1	2	1	1
Formaldehyde dehydrogenase		1.2.1.46	0	2	2	2	1	0
5-Carboxymethyl-2-hydroxymuconate semialdehyde Dehydrogenase		1.2.1.60	0	1	1	1	1	1
2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase		1.3.1.28	1	1	2	1	2	0
15-Oxoprostaglandin 13-Oxidase		1.3.1.48	2	1	3	3	3	1
Cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenase		1.3.1.56	0	2	1	0	0	0
Alanine dehydrogenase		1.4.1.1	1	1	1	1	1	1
Glutamic Dehydrogenase	Glutamate dehydrogenase (NAD(P+))	1.4.1.3	0	1	1	1	1	0
	Glutamate dehydrogenase (NADP(+))	1.4.1.4	0	1	1	1	1	0
Tetrahydrofolate dehydrogenase	Methylenetetrahydrofolate dehydrogenase (NADP(+))	1.5.1.5	1	2	2	1	0	1
	Formyltetrahydrofolate dehydrogenase	1.5.1.6	1	0	0	2	2	1
Saccharopine Dehydrogenase (NADP+, L-glutamate-forming)		1.5.1.10	1	1	1	1	1	1
1-Pyrroline-5-carboxylate dehydrogenase		1.5.1.12	0	2	1	2	1	1
Methylenetetrahydrofolate dehydrogenase (NAD(+))		1.5.1.15	1	1	1	1	1	0
Opine dehydrogenase		1.5.1.28	0	1	0	1	1	0
Proline dehydrogenase		1.5.99.8	0	1	1	2	1	0
NAD(P)H dehydrogenase (quinone)		1.6.5.2	0	1	1	1	1	0
NADPH dehydrogenase		1.6.99.1	1	9	7	3	6	0
NADH dehydrogenase (Quinone)		1.6.99.5	7	7	7	7	7	7
Dihydrolipoyl dehydrogenase		1.8.1.4	4	9	8	8	4	6
Xanthine dehydrogenase		1.17.1.4	1	1	1	1	1	1
Total			103	271	252	216	209	76

Protein families significantly under-represented (>2-fold) in *O. sinensis* are highlighted in bold.

Table S8 The core proteins involved in the biosynthesis of secondary metabolites in *O. sinensis* and other insect pathogens

Core enzyme ^a	<i>O. sinensis</i>	<i>C. militaris</i>	<i>B. bassiana</i>	<i>M. roberstii</i>	<i>M. acridum</i>
NRPS	6	7	14	11	10
NRPS-t1PKS	0	1	1	0	0
NRPS-Terpene	0	0	0	1	1
t1PKS	7	7	9	17	10
t1PKS-NRPS	1	5	5	8	5
t1PKS-Terpene	0	0	0	2	0
t1PKS-Terpene-NRPS	0	0	0	0	1
t3PKS	0	0	1	0	0
Terpene synthase	10	4	6	9	6
Terpene-NRPS	0	0	1	1	0
Other enzymes	6	6	5	12	7
Sum	30	30	42	61	40

^aAbbreviations: NRPS, non-ribosomal peptide synthetase; PKS, polyketide synthase; t1, type I; t3, type III. Other enzymes for either NRPS-like or PKS-like proteins.

Table S9 Comparison of proteins putatively involved in cold responses in *O. sinensis* and other insect pathogens

Function	Description	<i>O. sinensis</i>	<i>C. militaris</i>	<i>B. bassiana</i>	<i>M. roberstii</i>	<i>M. acridum</i>
Triacylglycerol accumulation	Aquaporin	1	1	1	1	1
	Glycerol kinase	2	1	1	2	2
	Phospholipid/glycerol acyltransferase	3	4	2	5	5
	Membrane bound O-acyl transferase	4	4	4	4	4
	Phosphatidic acid phosphatase type 2/haloperoxidase	4	6	6	6	6
	Diacylglycerol kinase	1	1	1	1	2
	Pyruvate kinase	4	7	5	7	6
	Perilipin-like protein	1	1	1	1	1
	Lipase	22	38	43	47	41
Fatty acid accumulation	Fatty acid desaturase	7	3	3	4	2
	Fatty acid synthase	1	1	1	2	2
	Fatty acid hydroxylase	6	15	15	14	11
Mannitol accumulation	Mannitol dehydrogenase	1	1	1	1	1
	Mannitol 1-phosphate 5-dehydrogenase, MPD	1	1	1	1	1
	Hexokinase, HXK	4	5	4	4	4
Trehalose accumulation	Trehalose-6-phosphate synthase/trehalose phosphatase (TPS/TPP)	2	3	5	2	2
	Trehalase	2	2	2	2	2
Heat response	Heat shock factor binding 1	2	2	3	2	1
	Heat shock protein HSP40	17	25	27	25	25
	Heat shock protein Hsp20	4	3	5	5	6
	Heat shock protein Hsp70	10	9	11	5	6
	Heat shock protein Hsp90	1	1	1	1	1
Cold response	Insect-like antifreeze protein	2	0	0	0	0
	Type II antifreeze protein	5	4	3	4	5
	RNA binding protein	1	1	1	2	2

Protein families significantly over- or under-represented in *O. sinensis* are highlighted in bold. Some bacteria and plants rely on antifreeze polyols such as trehalose and mannitol, but the *O. sinensis* genome encoded similar numbers of genes for these as other fungi.